GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:24 ; Search time 145.84 Seconds
(without alignments)
200.305 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275
Perfect score: 1343
Sequence: 1 YDIGEELGSGQFAIVKKCRE.....LVKETRKRLTIQEALRHPWI 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
18: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1343	100.0	360	21	AAY44674	Human DAP-kinase-r
2	1278	95.2	359	22	ABG09274	Novel human diagno
3	1121	83.5	454	20	AAY06921	Human ZIP-kinase (
4	1121	83.5	454	22	AAM93338	Human polypeptide,
5	1117	83.2	454	22	AAB94378	Human protein sequ
6	1117	83.2	454	22	AAG67425	Amino acid sequenc
7	1106	82.4	448	20	AAY06922	Murine ZIP-kinase
8	1079	80.3	1423	16	AAR74205	Human death associ
9	1079	80.3	1423	19	AAW71367	Death associated p
10	649	48.3	260	20	AAY43924	Chicken protein ki
11	638	47.5	414	20	AAY27161	Human DRAK1 protei
12	638	47.5	414	22	AAB65625	Novel protein kina
13	634	47.2	372	22	AAB65624	Novel protein kina
14	627.5	46.7	7107	22	ABB58144	Drosophila melanog
15	625	46.5	372	20	AAY27162	Human DRAK2 protei
16	625	46.5	372	22	AAB65623	Novel protein kina
17	617.5	46.0	291	22	AAB85502	Human protein kina
18	611.5	45.5	839	21	AAB56864	Human prostate can
19	599.5	44.6	814	22	AAB65634	Novel protein kina
20	599.5	44.6	819	20	AAY42111	Human ischaemic he
21	596.5	44.4	413	22	AAB65652	Novel protein kina
22	574	42.7	913	22	ABB62810	Drosophila melanog
23	574	42.7	913	22	ABB65968	Drosophila melanog
24	574	42.7	1289	20	AAY27163	Peptide Seq ID No:
25	574	42.7	1289	21	AAY56781	Human Trad protein
26	571.5	42.6	261	20	AAY43923	Rabbit protein kin
27	569.5	42.4	612	22	AAU03521	Human protein kina
28	559.5	41.7	596	22	AAG67544	Amino acid sequenc
29	553	41.2	450	22	ABG08502	Novel human diagno
30	542.5	40.4	307	18	AAW34892	Novel human phosph
31	542.5	40.4	307	20	AAW76803	Human phosphorylas
32	542.5	40.4	307	21	AAY52303	Novel human phosph
33	541	40.3	26926	22	AAU05396	Human titin (conne
34	525	39.1	638	22	ABB58483	Drosophila melanog
35	514	38.3	355	22	AAE11777	Human kinase (PKIN
36	514	38.3	355	22	AAM41268	Human polypeptide
37	514	38.3	355	22	AAB50055	Murine Dendritic C
38	514	38.3	356	22	AAB84360	Amino acid sequenc
39	514	38.3	357	22	AAE11768	Human kinase (PKIN
40	514	38.3	357	22	AAU03508	Human protein kina
41	514	38.3	385	22	AAM39482	Human polypeptide
42	514	38.3	385	22	AAB84359	Amino acid sequenc
43	508	37.8	493	22	ABB65515	Drosophila melanog
44	508	37.8	493	22	ABB66655	Drosophila melanog
45	508	37.8	493	22	ABB66656	Drosophila melanog

ALIGNMENTS

RESULT 1
AAY44674
ID AAY44674 standard; Protein; 360 AA.
XX
AC AAY44674;
XX
DT 18-APR-2000 (first entry)
XX
DE Human DAP-kinase-related protein 1 (DRP-1).
XX
KW DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;
KW calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;
KW cytostatic; antipsoriatic; immunosuppressive; metastasis; tumour; human;
KW treatment; cancer; psoriasis; autoimmune disease; screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 13..275
FT /label= Serine/Threonine_kinase_domain
FT Domain 292..320
FT /label= Calmodulin_regulatory_domain
FT Region 321..360
FT /label= C-terminal_region
FT /note= "Critical for DRP-1 dimerisation and apoptotic
FT induction"
XX
PN WO9966030-A1.
XX
PD 23-DEC-1999.
XX
PF 15-JUN-1999; 99WO-US13411.
XX
PR 15-JUN-1998; 98US-0089294.

XX
PA (YEDA) YEDA RES & DEV CO LTD.
PA (MCIN/) MCINNIS P A.
XX
PI Kimchi A;
XX
DR WPI; 2000-147148/13.
DR N-PSDB; AAZ49765.
XX
PT Calmodulin-dependent serine/threonine kinase capable of inducing
PT apoptosis used in the treatment of e.g. cancer -
XX
PS Claim 1; Fig 1; 67pp; English.
XX
CC The present sequence is DAP (death-associated protein)-kinase-related
CC protein 1 (DRP-1), which is a calmodulin-dependent serine/threonine
CC kinase. DRP-1 is a cytoplasmic protein capable of inducing apoptosis
CC by dimerisation. It shows significant homology to DAP kinase. It has
CC cytostatic, antipsoriatic and immunosuppressive activity and can be
CC used for inhibiting growth/metastasis of tumours and promoting
CC death of tumour cells. It can also be used in the treatment of cancer,
CC psoriasis and autoimmune diseases. Fragments of DRP-1 DNA are useful as
CC probes for screening individuals with a predisposition to cancer.
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1343; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.1e-127;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 ydigeelgsgqfaivkkcrekstgleyaakfikkrqsrasrrgvsreeierevsilrqvl 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 hhnvitlhdvyenrtdvvhilelvsggelfdflaqkeslseeeatsfikqildgvnylht 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 kkiahfdlkpenimlldknipiphiklidfglaheiedgvefknifgtpefvapeivnye 192

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 plgleadmwsigvityillsgaspflgdtkqetlanitsvsydfdeeffshtselakdfi 252

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
          |||||||||||||||||||||||
Db     253 rkllvketrkrltiqealrhpwi 275
```

RESULT 2
ABG09274
ID ABG09274 standard; Protein; 359 AA.
XX
AC ABG09274;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #9265.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS73461.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 39633; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 359 AA;

Query Match 95.2%; Score 1278; DB 22; Length 359;
Best Local Similarity 98.8%; Pred. No. 4.2e-121;
Matches 252; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy       9 SGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVLHHNVITLH 68
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 sgqfaivkkcrekstgleyaakfikkrqsrasrrgvsreeierevsilrqvlhhnvitlh 79

Qy      69 DVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHTKKIAHFDL 128
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 dvyenrtdvvlilelvsggelfdflaqkeslseeeatsfikqildgvnylhtkkiahfdl 139

Qy     129 KPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYEPLGLEADM 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 kpenimlldknipiphiklidfglaheiedgvefknifgtpefvapeivnyeplgleadm 199

Qy     189 WSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFIRKLLVKET 248
          |||||||||||||||||||||||||||||:|||||||||| ||||||||||||||||||||
Db     200 wsigvityillsgaspflgdtkqetlanitavsydfdeeffsqtselakdfirkllvket 259

Qy     249 RKRLTIQEALRHPWI 263
          |||||||||||||||
Db     260 rkrltiqealrhpwi 274
```

RESULT 3
AAY06921
ID AAY06921 standard; Protein; 454 AA.
XX
AC AAY06921;
XX

DT 01-JUL-1999 (first entry)
XX
DE Human ZIP-kinase (serine/threonine kinase).
XX
KW Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
KW human; murine.
XX
OS Homo sapiens.
XX
PN EP911408-A2.
XX
PD 28-APR-1999.
XX
PF 24-SEP-1998; 98EP-0307747.
XX
PR 26-SEP-1997; 97JP-0261589.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Akira S, Kawai T;
XX
DR WPI; 1999-246420/21.
DR N-PSDB; AAX34656.
XX
PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
PT protein and DNA, useful as anticancer agents
XX
PS Claim 1; Page 15-18; 33pp; English.
XX
CC The invention provides human and murine recombinant Zipper Interacting
CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
CC kinases which bind the leucine zipper domain of transcription factor
CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
CC acids are used for the recombinant expression of the proteins. ZIP-kinase
CC protein and DNA are useful as gene therapeutic agents against cancer, and
CC as anti-cancer agents. The present sequence represents a human ZIP kinase
CC protein.
XX
SQ Sequence 454 AA;

Query Match 83.5%; Score 1121; DB 20; Length 454;
Best Local Similarity 79.8%; Pred. No. 4.9e-105;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

```
Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
           |::|||||||||||||:|||:| || ||||||||||:  :|||||||||||||:|||::
Db      13 yemgeelgsgqfaivrkcrqkgtgkeyaakfikkrrlsssrrgvsreeierevnilreir 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
           | |:|||||::||:|||| ||||||||||||||:||||:|:||| |:|||||||:|||:
Db      73 hpniitlhdifenktdvvlilelvsggelfdflaekesltedeatqflkqildgvhylhs 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
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Db     133 kriahfdlkpenimlldknvpnpriklidfgiahkieagnefknifgtpefvapeivnye 192

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
           ||||||||||||||||||||||||||:|||||| ||::|:|||||||:||:|||||||||
Db     193 plgleadmwsigvityillsgaspflgetkqetltnisavnydfdeeyfsntselakdfi 252

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
           |:||||: ::|:|| ::| | ||
Db     253 rrllvkdpkrrmtiaqslehswi 275
```

RESULT 4
AAM93338
ID AAM93338 standard; Protein; 454 AA.
XX
AC AAM93338;
XX

DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 2875.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94258.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 2875; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 454 AA;

Query Match 83.5%; Score 1121; DB 22; Length 454;
Best Local Similarity 79.8%; Pred. No. 4.9e-105;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

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Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
           |::|||||||||||||:|||:| || ||||||||||:  :|||||||||||||:|||::
Db      13 yemgeelgsgqfaivrkcrqkgtgkeyaakfikkrrlsssrrgvsreeierevnilreir 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
           | |:|||||::||:|||| ||||||||||||||:||||:|:||| |:|||||||:|||:
Db      73 hpniitlhdifenktdvvlilelvsggelfdflaekesltedeatqflkqildgvhylhs 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
           |:|||||||||||||||:| | ||||||||:||:|| | ||||||||||||||||||||
Db     133 kriahfdlkpenimlldknvpnpriklidfgiahkieagnefknifgtpefvapeivnye 192

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
           ||||||||||||||||||||||||||:|||||| ||::|:|||||||:||:|||||||||
Db     193 plgleadmwsigvityillsgaspflgetkqetltnisavnydfdeeyfsntselakdfi 252

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
           |:||||: ::|:|| ::| | ||
Db     253 rrllvkdpkrrmtiaqslehswi 275
```

RESULT 5

AAB94378
ID AAB94378 standard; Protein; 454 AA.
XX
AC AAB94378;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:14926.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 14926; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 454 AA;

Query Match 83.2%; Score 1117; DB 22; Length 454;
Best Local Similarity 79.5%; Pred. No. 1.2e-104;
Matches 209; Conservative 36; Mismatches 18; Indels 0; Gaps 0;

```
Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
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Db      13 yemgeelgsgqfaivrkcrqkgtgkeyaakfikkrrlsssrrgvsreeierevnilreir 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
           | |:||||::||:|||| ||||||||||||||:||||:|:||| |:||||||:|||:
Db      73 hpniitlhdifenktdvvlilelvsggelfdflaekesltedeatqflkqildgvhylhs 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
           |:|||||||||||||||:| | |||||||:||:|| | ||||||||||||||||||||
Db     133 kriahfdlkpenimlldknvpnpriklidfgiahkieagnefknifgtpefvapeivnye 192

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
           ||||||||||||||||||||||||||:|||||| ||:::|:|||||:||:| |||||||
Db     193 plgleadmwsigvityillsgaspflgetkqetltnisavnydfdeeyfsntgelakdfi 252

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
           |:|||: ::|:|| ::| | ||
Db     253 rrllvkdpkrrmtiaqslehswi 275
```

RESULT 6
AAG67425
ID AAG67425 standard; Protein; 454 AA.
XX
AC AAG67425;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a human protein kinase/protein phosphatase.
XX
KW Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX
OS Homo sapiens.
XX
PN WO200109345-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-JP05060.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI; 2001-564736/63.
DR N-PSDB; AAH78068.
XX
PT New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
XX
PS Claim 2; Page 125-128; 336pp; Japanese.
XX
CC The present sequence represents a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules fir drug development.
XX
SQ Sequence 454 AA;

Query Match 83.2%; Score 1117; DB 22; Length 454;
Best Local Similarity 79.5%; Pred. No. 1.2e-104;

Matches 209; Conservative 36; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
          |::|||||||||||||:|||:| || ||||||||||:  :|||||||||||||||:|||::
Db     13 yemgeelgsgqfaivrkcrqkgtgkeyaakfikkrrlsssrrgvsreeierevnilreir 72

Qy     61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
          | |:|||||::||:|||| ||||||||||||||:||||:|:||| |:|||||||:|||:
Db     73 hpniitlhdifenktdvvlilelvsggelfdflaekesltedeatqflkqildgvhylhs 132

Qy    121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
          |:|||||||||||||||||:| | |||||||:||:|| | ||||||||||||||||||||
Db    133 kriahfdlkpenimlldknvpnpriklidfgiahkieagnefknifgtpefvapeivnye 192

Qy    181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
          ||||||||||||||||||||||||||||:|||||| ||::|:||||||:||:| |||||||
Db    193 plgleadmwsigvityillsgaspflgetkqetltnisavnydfdeeyfsntgelakdfi 252

Qy    241 RKLLVKETRKRLTIQEALRHPWI 263
          |:||||: ::|:|| ::| | ||
Db    253 rrllvkdpkrrmtiaqslehswi 275
```

RESULT 7
AAY06922
ID AAY06922 standard; Protein; 448 AA.
XX
AC AAY06922;
XX
DT 01-JUL-1999 (first entry)
XX
DE Murine ZIP-kinase (serine/threonine kinase).
XX
KW Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
KW human; murine.
XX
OS Mus musculus.
XX
PN EP911408-A2.
XX
PD 28-APR-1999.
XX
PF 24-SEP-1998; 98EP-0307747.
XX
PR 26-SEP-1997; 97JP-0261589.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Akira S, Kawai T;
XX
DR WPI; 1999-246420/21.
DR N-PSDB; AAX34657.
XX
PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
PT protein and DNA, useful as anticancer agents
XX
PS Claim 2; Page 19-22; 33pp; English.
XX
CC The invention provides human and murine recombinant Zipper Interacting
CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
CC kinases which bind the leucine zipper domain of transcription factor
CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
CC acids are used for the recombinant expression of the proteins. ZIP-kinase
CC protein and DNA are useful as gene therapeutic agents against cancer, and
CC as anti-cancer agents. The present sequence represents a murine ZIP
CC kinase protein.
XX
SQ Sequence 448 AA;

Query Match 82.4%; Score 1106; DB 20; Length 448;
Best Local Similarity 79.5%; Pred. No. 1.6e-103;

Matches 209; Conservative 34; Mismatches 20; Indels 0; Gaps 0;

```
Qy      1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
          |::|||||||||||||:||::| ||:|||||||||:  :|||||||||||||||||::
Db     13 yemgeelgsgqfaivrkcqqkgtgmeyaakfikkrrlpssrrgvsreeierevsilreir 72

Qy     61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
          | |:||||||:||:|||| ||||||||||||||:||||:|:||| |:|||||||:|||:
Db     73 hpniitlhdvfenktdvvlilelvsggelfdflaekesltedeatqflkqildgvhylhs 132

Qy    121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
          |:|||||||||||||||:   | |||||||:|| || | ||||||||||||||||||||
Db    133 kriahfdlkpenimlldkhaaspriklidfgiahrieagsefknifgtpefvapeivnye 192

Qy    181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
          ||||||||||||||||||||||||||||:|||||| ||::|:||||||:|| |||||||||
Db    193 plgleadmwsigvityillsgaspflgetkqetltnisavnydfdeeyfsstselakdfi 252

Qy    241 RKLLVKETRKRLTIQEALRHPWI 263
          |:||||: ::|:|| ::| | ||
Db    253 rrllvkdpkrrmtiaqslehswi 275
```

RESULT 8
AAR74205
ID AAR74205 standard; Protein; 1423 AA.
XX
AC AAR74205;
XX
DT 04-JAN-1980 (first entry)
XX
DE Human death associated protein DAP-2.
XX
KW Death associated protein; DAP; cytokine; cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 13..267
FT /label= protein kinase domain
FT Region 280..312
FT /label= calmodulin regulatory region
FT Domain 365..629
FT /label= ankyrin repeats domain
FT Region 365..397
FT /label= ar1
FT /note= "ankyrin repeat 1"
FT Region 398..431
FT /label= ar2
FT Region 432..464
FT /label= ar3
FT Region 466..497
FT /label= ar4
FT Region 498..530
FT /label= ar5
FT Region 531..563
FT /label= ar6
FT Region 564..596
FT /label= ar7
FT Region 597..629
FT /label= ar8
FT Region 631..638
FT /label= p-loop 1
FT Region 587..594
FT /label= p-loop 2
XX
PN WO9510630-A.
XX
PD 20-APR-1995.
XX
PF 12-OCT-1994; 94WO-US11598.
XX
PR 12-OCT-1993; 93IL-0107250.

```
XX
PA   (RYCU/) RYCUS A.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Kimchi A;
XX
DR   WPI; 1995-178528/23.
DR   N-PSDB; AAQ89838, AAQ89839.
XX
PT   DNA whose expression mediates cytokine-induced programmed cell
PT   death  - used to treat diseases or disorders associated with
PT   uncontrolled, pathological cell growth or cytokine-induced
PT   programmed cell death.
XX
PS   Claim 8; Fig 8; 61pp; English.
XX
CC   DAP genes seem to play an imp. role in programmed cell death and the
CC   inhibition of their expression protects the cell from cytokine-
CC   promoted cell death. A cDNA library was generated from a mixture of
CC   mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
CC   was cloned in antisense orientation into the EBV-based pTK01
CC   expression vector. The resulting expression library was introduced
CC   into HeLa cells. A fraction of the transfectants was selected with
CC   hygromycin B. The majority of transfected cells were selected with
CC   both hygromycin B and IFN-gamma. The cells that survived and/or
CC   grew in the presence of IFN-gamma were expanded and pooled. The
CC   extrachromosomal DNA was obtd. and cleaved with DpnI and introduced
CC   into E. coli HB101 host cells. A few bacterial clones were obtd.
CC   which included DNA antisense sequences, some of which were able to
CC   protect cells from the death-promoting effects of IFN-gamma.
CC   Plasmid DNAs were prepd. from 10 individual bacterial clones. PCR
CC   amplified cDNA inserts were generated from each plasmid using
CC   primers that corresp. to the immediate flanking sequence of the
CC   cDNA insertion sites in the pTK01 vector. The PCR fragments were
CC   used as labeled probes to seach Southern blots for possible cross
CC   hybridisation between some of the rescued antisense cDNA clones.
CC   The 10 cDNA clones were classified into six distinct
CC   non-overlapping gps., some constituting several members (clones)
CC   and some constituting a single member. Antisense cDNA clone 256 has
CC   the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
CC   used to screen a K562 lambda gt10 cDNA library. The resulting
CC   composite sequence derived from 2 clones and the deduced AA sequence
CC   are shown in AAQ89838 and AAR74205. The ORF is also shown in AAQ89839.
CC   AAQ89838 has a poly A tail. The calculated mol. wt. of the protein
CC   is about 160 kDa. Several known domains and motifs were identified
CC   in the protein (see AAQ74205 FT).
XX
SQ   Sequence   1423 AA;

  Query Match             80.3%;  Score 1079;  DB 16;  Length 1423;
  Best Local Similarity   77.2%;  Pred. No. 4.5e-100;
  Matches  203;  Conservative   39;  Mismatches   13;  Indels    8;  Gaps    1;

Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
           || |||||||||||:|||||||||||:| |||||||:::::||||||||:|||||||:::
Db      13 ydtgeelgsgqfavvkkcrekstglqypakfikkrrtkssrrgvsredierevsilkeiq 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
           | ||||||:||||:|||: |||||:|||||||||:||||:||||| |:||||:|| |||:
Db      73 hpnvitlhevyenktdvililelvaggelfdflaekeslteeeateflkqilngvyylhs 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
           :|||||||||||||||:|:| | ||:|||        | ||||||||||||||||||||
Db     133 lqiahfdlkpenimlldrnvpkprikiidf--------gnefknifgtpefvapeivnye 184

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
           |||||||||||||||||||||||||||||||||||:::|:|:|:::|:||:|| ||||||
Db     185 plgleadmwsigvityillsgaspflgdtkqetlanvsavnyefedeyfsntsalakdfi 244

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
           |:|||: :||:|||::|:|||||
Db     245 rrllvkdpkkrmtiqdslqhpwi 267
```

```
RESULT   9
AAW71367
ID   AAW71367 standard; Protein; 1423 AA.
XX
AC   AAW71367;
XX
DT   12-JAN-1999  (first entry)
XX
DE   Death associated protein-2 (DAP-1, DAP-kinase).
XX
KW   Death associated protein; DAP-2; cell death; tumour cell; DAP-kinase;
KW   metastatic activity; cancer; psoriasis; autoimmune disease;
KW   programmed cell death; degenerative neurological disease;
KW   Alzheimer's.
XX
OS   Homo sapiens.
XX
PN   WO9839429-A2.
XX
PD   11-SEP-1998.
XX
PF   03-MAR-1998;   98WO-IL00102.
XX
PR   03-MAR-1997;   97US-0810712.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Kimchi A;
XX
DR   WPI; 1998-520781/44.
DR   N-PSDB; AAV60289.
XX
PT   New isolated death associated protein nucleic acids - used for the
PT   diagnosis and treatment or disorders associated with programmed cell
PT   death, e.g. cancers, auto:immune disease or neurological disease
XX
PS   Disclosure; Fig 8; 157pp; English.
XX
CC   The present sequence represents a death associated protein-2 (DAP-2,
CC   DAP-kinase). The DAP genes and proteins are used for promoting death of
CC   normal or tumour cells, and for suppressing the metastatic activity of
CC   tumour cells. They can be used in the treatment of diseases or disorders
CC   associated with uncontrolled pathological growth, e.g. cancer,
CC   psoriasis, autoimmune diseases and others. Agents which antagonise,
CC   inhibit or nuetralize DAP products are used for protecting cells from
CC   programmed cell death. In this case they can be used for the treatment
CC   of degenerative neurological diseases, e.g. Alzheimer's, prevention of
CC   death of T cells in AIDS patients, prevention of rejection associated
CC   cell death in transplants, and protection of normal cells from
CC   the cytotoxic effects of anti-cancer therapies.
XX
SQ   Sequence   1423 AA;

  Query Match             80.3%;  Score 1079;  DB 19;  Length 1423;
  Best Local Similarity   77.2%;  Pred. No. 4.5e-100;
  Matches  203;  Conservative   39;  Mismatches   13;  Indels    8;  Gaps    1;

Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
           || |||||||||||:|||||||||||:| |||||||:::::||||||||:|||||||:::
Db      13 ydtgeelgsgqfavvkkcrekstglqypakfikkrrtkssrrgvsredierevsilkeiq 72

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
           | ||||||:||||:|||: |||||:|||||||||:||||:||||| |:||||:|| |||:
Db      73 hpnvitlhevyenktdvililelvaggelfdflaekeslteeeateflkqilngvyylhs 132

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
           :|||||||||||||||:|:| | ||:|||        | ||||||||||||||||||||
Db     133 lqiahfdlkpenimlldrnvpkprikiidf--------gnefknifgtpefvapeivnye 184

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
```

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          ||||||||||||||||||||||||||||||||||:::|:|:|::|:||:|| ||||||
Db    185 plgleadmwsigvityillsgaspflgdtkqetlanvsavnyefedeyfsntsalakdfi 244

Qy    241 RKLLVKETRKRLTIQEALRHPWI 263
          |:|||||: :|||:|||::|:|||
Db    245 rrllvkdpkkrmtiqdslqhpwi 267


RESULT  10
AAY43924
ID   AAY43924 standard; Protein; 260 AA.
XX
AC   AAY43924;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Chicken protein kinase #1.
XX
KW   Prediction; secondary structure; alignment; evolutionary conservation;
KW   homology; periodicity; co-variation analysis; antigenic site;
KW   site directed mutagenesis; interaction.
XX
OS   Gallus sp.
XX
PN   US5958784-A.
XX
PD   28-SEP-1999.
XX
PF   25-MAR-1992;   92US-0857224.
XX
PR   25-MAR-1992;   92US-0857224.
XX
PA   (BENN/) BENNER S A.
XX
PI   Benner SA;
XX
DR   WPI; 1999-570766/48.
XX
PT   Predicting the folded structure of proteins  -
XX
PS   Disclosure; Column 181-182; 113pp; English.
XX
CC   Sequences AAY43902-Y44015 represent proteins used in a novel method of
CC   predicting the folded structure of proteins, by aligning sequences of
CC   homologous proteins and using patterns of evolutionarily conserved and
CC   varied sequences to assign positions. Positions in the alignment are
CC   assigned to the surface or inside of the folded structure, active sites,
CC   and parsing segments. Secondary structural units are assigned by
CC   identifying periodicity in the assignments,  and assembled into globular
CC   form using distance constraints imposed by disulfide bridges, active
CC   site assignments and co-variation analysis. The predicted secondary
CC   structures are useful for identifying antigenic sites on a protein
CC   molecule, as guides for site directed mutagenesis studies, and for
CC   understanding the interaction of a protein with other molecules.
XX
SQ   Sequence   260 AA;


  Query Match             48.3%;  Score 649;  DB 20;  Length 260;
  Best Local Similarity   47.9%;  Pred. No. 1.6e-57;
  Matches  126;  Conservative   48;  Mismatches   81;  Indels    8;  Gaps    2;

Qy      1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
          |:| | ||||:|  | :  || ||  :| || |   ::       :| |  |:||:  :
Db      3 ynieerlgsgkfgqvfrlvekktgkvwagkffkaysak------ekenirdeisimnclh 56

Qy     61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT 120
          |  ::   | :| : ::| :||:|||||||: :  :: |:| |   :::|| :|| |:|
Db     57 hpklvqcvdafeekanivmvlemvsggelferiidedflterecikymrqisegveyihk 116

Qy    121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
          : | | |||||||| ::|      |||||||||  :|     | :|||||||||::|||
Db    117 qgivhldlkpenimcvnkt--gtsiklidfglarrlesagslkvlfgtpefvapevinye 174

Qy    181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
          |:| | ||||||||  |||:|| |||:||   |||||:|| :: ||:| |   |: |||||
Db    175 pigyetdmwsigvicyilvsglspfmgdndnetlanvtsatwtfddeafdeisddakdfi 234

Qy    241 RKLLVKETRKRLTIQEALRHPWI 263
            || |: : ||   : |:|||:
Db    235 snllkkdmksrlnctqclqhpwl 257


RESULT  11
AAY27161
ID   AAY27161 standard; Protein; 414 AA.
XX
AC   AAY27161;
XX
DT   15-SEP-1999  (first entry)
XX
DE   Human DRAK1 protein.
XX
KW   DRAK1; DRAK2; DAP kinase related apoptosis inducing kinase; human;
KW   apoptosis; breast cancer; ovarian cancer; lymphoma; autoimmune disease;
KW   viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease;
KW   Parkinson's disease; arteriosclerosis; alcoholism; rheumatoid arthritis;
KW   diabetes.
XX
OS   Homo sapiens.
XX
PN   WO9933961-A1.
XX
PD   08-JUL-1999.
XX
PF   25-DEC-1998;   98WO-JP05974.
XX
PR   17-APR-1998;   98JP-0108150.
PR   26-DEC-1997;   97JP-0367640.
PR   26-DEC-1997;   97JP-0367641.
PR   17-APR-1998;   98JP-0108149.
XX
PA   (ASAH ) ASAHI KASEI KOGYO KK.
XX
PI   Akira S,  Kawai T;
XX
DR   WPI; 1999-430239/36.
DR   N-PSDB; AAX89196.
XX
PT   New kinase with apoptosis induction activity useful in the treatment
PT   of cancer, autoimmune diseases and viral infections
XX
PS   Claim 2; Page 134-137; 180pp; Japanese.
XX
CC   The invention provides kinases DRAK1 and DRAK2 (DAP kinase related
CC   apoptosis inducing kinase) having apoptosis inducing activity. The
CC   kinases can be expressed recombinantly by transforming host cells with
CC   vectors comprising the nucleic acids encoding the kinases. The kinases
CC   are useful in the treatment, prevention, diagnosis and investigation of
CC   diseases with which apoptosis is associated, such as hormonally regulated
CC   cancer (such as breast cancer, ovarian cancer, lymphoma); autoimmune
CC   diseases; viral infections (such as herpes, adenovirus, poxvirus, HIV);
CC   Alzheimer's disease; Parkinson's disease; arteriosclerosis; alcoholism;
CC   rheumatoid arthritis; and diabetes. The present sequence represents the
CC   human DRAK1 amino acid sequence.
XX
SQ   Sequence   414 AA;


  Query Match             47.5%;  Score 638;  DB 20;  Length 414;
  Best Local Similarity   46.0%;  Pred. No. 4.2e-56;
  Matches  122;  Conservative   65;  Mismatches   66;  Indels   12;  Gaps    6;

Qy      4 GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REEIEREVSILRQVLHH 62
          | ||| |:||:|:|| :| :| |:||||::||     |:|   | ||  |:::| ::
Db     64 grelgrgkfavvrkcikkdsgkefaakfmrkr-----rkgqdcrmeiiheiavl-elaqd 117
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```
Qy      63 N--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEEEATSFIKQILDGVNYL 118
           |  || ||:|||  :::: :||  :|||:||     ::|:  |::    ::|||:||::|
Db     118 npwvinlhevyetasemilvleyaaggeifdqcvadreeafkekdvqrlmrqilegvhfl 177

Qy     119 HTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN 178
           ||: : | ||||:||:|  :: |:  ||::||||:  :::  | : | ||||:|||||:: 
Db     178 htrdvvhldlkpqnilltses-plgdikivdfglsrilknseelreimgtpeyvapeils 236

Qy     179 YEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKD 238
           |:|: :  |||||||:||::|:| |||||: |||| ||: ::  : || |  || | |
Db     237 ydpismatdmwsigvltyvmltgispflgndkqetflnisqmnlsyseeefdvlsesavd 296

Qy     239 FIRKLLVKETRKRLTIQEALRHPWI 263
           ||| ||||:   | | :| |:|||:
Db     297 firtllvkkpedrataeeclkhpwl 321
```

RESULT 12
AAB65625
ID AAB65625 standard; Protein; 414 AA.
XX
AC AAB65625;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 151.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14842.
XX
PR 28-MAY-1999; 99US-0136503.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44651.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
PS Claim 10; Fig 1; 310pp; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
XX
SQ Sequence 414 AA;

Query Match 47.5%; Score 638; DB 22; Length 414;
Best Local Similarity 46.0%; Pred. No. 4.2e-56;
Matches 122; Conservative 65; Mismatches 66; Indels 12; Gaps 6;

```
Qy       4 GEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REEIEREVSILRQVLHH 62
           | ||| |:||:|:|| :| :| |:||||::||     |:|   | ||  |:::| ::
Db      64 grelgrgkfavvrkcikkdsgkefaakfmrkr-----rkgqdcrmeiiheiavl-elaqd 117

Qy      63 N--VITLHDVYENRTDVVHILELVSGGELFD--FLAQKESLSEEEATSFIKQILDGVNYL 118
           |  || ||:|||  :::: :||  :|||:||     ::|:  |::    ::|||:||::|
Db     118 npwvinlhevyetasemilvleyaaggeifdqcvadreeafkekdvqrlmrqilegvhfl 177

Qy     119 HTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN 178
           ||: : | ||||:||:|  :: |:  ||::||||:  :::  | : | ||||:|||||:: 
Db     178 htrdvvhldlkpqnilltses-plgdikivdfglsrilknseelreimgtpeyvapeils 236

Qy     179 YEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKD 238
           |:|: :  |||||||:||::|:| |||||: |||| ||: ::  : || |  || | |
Db     237 ydpismatdmwsigvltyvmltgispflgndkqetflnisqmnlsyseeefdvlsesavd 296

Qy     239 FIRKLLVKETRKRLTIQEALRHPWI 263
           ||| ||||:   | | :| |:|||:
Db     297 firtllvkkpedrataeeclkhpwl 321
```

RESULT 13
AAB65624
ID AAB65624 standard; Protein; 372 AA.
XX
AC AAB65624;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 150.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Mus musculus.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14842.
XX
PR 28-MAY-1999; 99US-0136503.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44650.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
PS Claim 10; Fig 1; 310pp; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and

```
CC   diagnosis of diseases associated with inappropriate kinase expression
CC   such as immune-related diseases and disorders, cardiovascular disease,
CC   neurodegenerative diseases and/or cancers. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays. The kinase polypeptides may be used as antigens in the production
CC   of antibodies of kinase expression and activity. Anti-kinase antibodies
CC   and kinase antagonists may also be used to down regulate kinase
CC   expression and activity. Diseases related to kinase expression and
CC   activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC   disorders, complications of organ transplantation, myocardial infarction,
CC   immune disorders, cardiomyopathies, strokes, renal failure,
CC   oxidative-stress related disorders, chronic inflammatory bowel disease,
CC   chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC   osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC   reproductive disorders.
XX
SQ   Sequence   372 AA;


  Query Match             47.2%;  Score 634;  DB 22;  Length 372;
  Best Local Similarity   48.3%;  Pred. No. 9.1e-56;
  Matches  128;  Conservative   49;  Mismatches   74;  Indels   14;  Gaps    6;

Qy       5 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REEIEREVSIL---RQVL 60
           :||| |:||:|::|  |||| ||||| :|||     |||   | ||  |:::|   |
Db      37 kelgrgkfavvrqciskstgqeyaakslkkr-----rrgqdcraeilheiavlelarscp 91

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQK--ESLSEEEATSFIKQILDGVNYL 118
           |  || ||:|||| |::: :||  :|||:|:    :  | :|| :    |||||:||:||
Db      92 h--vinlhevyenateiilvleyaaggeifnlclpelaemvsendvirlikqilegvhyl 149

Qy     119 HTKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVN 178
           |   | | ||||:|| ||    |:  ||::|||:: :| :  | : | ||||::||||:|
Db     150 hqnnivhldlkpqni-llssiyplgdikivdfgmsrkignaselreimgtpeylapeiln 208

Qy     179 YEPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKD 238
           |:|:    |||:||:| |:||:  |||:|:  |||  ||: |: |: || ||  |:|| |
Db     209 ydpittatdmwnigiiaymllthtspfvgednqetylnisqvnvdyseemfssvsqlatd 268

Qy     239 FIRKLLVKETRKRLTIQEALRHPWI 263
           ||: ||||   || | :  | | |:
Db     269 fiqsllvknpekrptaesclshswl 293


RESULT  14
ABB58144
ID   ABB58144 standard; Protein; 7107 AA.
XX
AC   ABB58144;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 1224.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL02247.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 1224; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   7107 AA;


  Query Match             46.7%;  Score 627.5;  DB 22;  Length 7107;
  Best Local Similarity   46.6%;  Pred. No. 2.7e-53;
  Matches  123;  Conservative   51;  Mismatches   81;  Indels    9;  Gaps    3;

Qy       1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
           ||| ||:|:| | :| :|||:|||  :|||||    |      | :: | ||: |: |:
Db    6138 ydileeigtgafgvvhrcrerstgnifaakfipvshs------vekdlirreidimnqlh 6191

Qy      61 HHNVITLHDVYENRTDVVHILELVSGGELFD-FLAQKESLSEEEATSFIKQILDGVNYLH 119
           |  :| ||| :|:  ::: ||| :|||||:   |:   ::| |  ::::|| :|: ::|
Db    6192 hqklinlhdafedddemililefisggelferitaegyvmteaevinymrqicegirhmh 6251

Qy     120 TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY 179
           : | | |:||||||   ::    ::|||||||| ::     |   || || ||||||
Db    6252 eqniihldikpenimcqtrs--stnvklidfglatrldpnevvkittgtaefaapeivnr 6309

Qy     180 EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF 239
           ||:|   |||: ||::|:|||| ||| ||   :|| |: :  :||| | | : || ||||
Db    6310 epvgfytdmwatgvlsyvllsglspfagdndvqtlknvkacdwdfdvesfkyiseeakdf 6369

Qy     240 IRKLLVKETRKRLTIQEALRHPWI 263
           ||||||:   ||:|  | | |||:
Db    6370 irkllvrnkekrmtahecllhpwl 6393


RESULT  15
AAY27162
ID   AAY27162 standard; Protein; 372 AA.
XX
AC   AAY27162;
XX
DT   15-SEP-1999  (first entry)
XX
DE   Human DRAK2 protein.
XX
KW   DRAK1; DRAK2; DAP kinase related apoptosis inducing kinase; human;
KW   apoptosis; breast cancer; ovarian cancer; lymphoma; autoimmune disease;
KW   viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease;
KW   Parkinson's disease; arteriosclerosis; alcoholism; rheumatoid arthritis;
KW   diabetes.
XX
OS   Homo sapiens.
XX
PN   WO9933961-A1.
XX
PD   08-JUL-1999.
XX
PF   25-DEC-1998;   98WO-JP05974.
XX
PR   17-APR-1998;   98JP-0108150.
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PR 26-DEC-1997; 97JP-0367640.
PR 26-DEC-1997; 97JP-0367641.
PR 17-APR-1998; 98JP-0108149.
XX
PA (ASAH) ASAHI KASEI KOGYO KK.
XX
PI Akira S, Kawai T;
XX
DR WPI; 1999-430239/36.
DR N-PSDB; AAX89198.
XX
PT New kinase with apoptosis induction activity useful in the treatment
PT of cancer, autoimmune diseases and viral infections
XX
PS Claim 2; Page 141-144; 180pp; Japanese.
XX
CC The invention provides kinases DRAK1 and DRAK2 (DAP kinase related
CC apoptosis inducing kinase) having apoptosis inducing activity. The
CC kinases can be expressed recombinantly by transforming host cells with
CC vectors comprising the nucleic acids encoding the kinases. The kinases
CC are useful in the treatment, prevention, diagnosis and investigation of
CC diseases with which apoptosis is associated, such as hormonally regulated
CC cancer (such as breast cancer, ovarian cancer, lymphoma); autoimmune
CC diseases; viral infections (such as herpes, adenovirus, poxvirus, HIV);
CC Alzheimer's disease; Parkinson's disease; arteriosclerosis; alcoholism;
CC rheumatoid arthritis; and diabetes. The present sequence represents the
CC human DRAK2 amino acid sequence.
XX
SQ Sequence 372 AA;

Query Match 46.5%; Score 625; DB 20; Length 372;
Best Local Similarity 48.3%; Pred. No. 7.4e-55;
Matches 127; Conservative 46; Mismatches 80; Indels 10; Gaps 5;

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Qy       5 EELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVS-REEIEREVSILRQVLH-H  62
           :||| |:||:|::|  |||| ||||||:|||     |||   | ||  |:::|
Db      37 kelgrgkfavvrqciskstgqeyaakflkkr-----rrgqdcraeilheiavlelakscp  91

Qy      63 NVITLHDVYENRTDVVHILELVSGGELFDFLAQK--ESLSEEEATSFIKQILDGVNYLHT 120
             || ||:|||| :::: |||  :|||:|     :  | :|| :    |||||:|| |||
Db      92 rvinlhevyentseiilileyaaggeifslclpelaemvsendvirlikqilegvyylhq 151

Qy     121 KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE 180
             | | ||||:|| ||    |:  ||::|||:: :|    | : | ||||::||||:|||:
Db     152 nnivhldlkpqni-llssiyplgdikivdfgmsrkighacelreimgtpeylapeilnyd 210

Qy     181 PLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDFI 240
           |:    |||:||:| |:||:  |||:|:  |||  ||: |: |: || ||  |:|| |||
Db     211 pittatdmwnigiiaymllthtspfvgednqetylnisqvnvdyseetfssvsqlatdfi 270

Qy     241 RKLLVKETRKRLTIQEALRHPWI 263
             : ||||   || | :  | | |:
Db     271 qsllvknpekrptaeiclshswl 293
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Job time: 18480 sec